Applicant: Ron S. Israeli, et al.

U.S. Serial No.: 08/466,381 Filing Date: June 6, 1995

Page: 2

1.121(b) by deleting the bracketed material and inserting the underlined material as follows:

- )97. (Amended) A method of detecting micrometastic prostate tumor cells in a subject which comprises:
  - a) obtaining a suitable sample of mRNA from the subject;
  - b) contacting the mRNA sample under hybridizing conditions with a labeled nucleic acid probe which:

     (1) is at least 15 nucleotides in length and (2)
     hybridizes specifically to a nucleic acid having a sequence which is complementary to a sequence present in the sequence set forth in SEQ ID NO. 1.
  - c) removing any unbound labeled nucleic acid probe; and
  - d) detecting the presence of labeled nucleic acid probe hybridized to the mRNA;
  - e) comparing the amount of labeled nucleic acid probe measured in step d) with an amount measured in a negative control sample which does not have micrometastic prostate tumor cells, wherein a higher amount measured in step d) compared to the amount measured in the control sample indicates the detection of [so as to thereby detect] micrometastic prostate tumor cells in the subject.-
- --98. (Amended) A method of detecting micrometastic prostate tumor cells in a subject which comprises:
  - a) obtaining a suitable sample of mRNA from the subject;
  - b) reverse transcribing the mRNA to generate a single

3

Applicants: Ron S. Israeli, et al.

Serial No.: 08/466,381 Filed : June 6, 1995

Page 3

-stranded cDNA;

- c) contacting the single-stranded cDNA under hybridizing conditions with a labeled nucleic acid probe which: 1) is at least 15 nucleotides in length; and 2) hybridizes specifically to a nucleic acid having a sequence set forth in SEQ ID NO:1;--
- d) removing any unbound labeled nucleic acid probe; and
- e) detecting the presence of labeled nucleic acid probe hybridized to the cDNA;
- f) comparing the amount of labeled nucleic acid probe measured in step e) with an amount measured in a negative control sample which does not have micrometastic prostate tumor cells, wherein a higher amount measured in step e) compared to the amount measured in the control sample indicates the detection of [so as to thereby detect detect] micrometastic prostate tumor cells in the subject.-

JI --99.

(Amended) A method of detecting micrometastic prostate tumor cells in a subject which comprises:

- a) obtaining a suitable sample of mRNA from the subject;
- b) generating a double-stranded mRNA-cDNA duplex from the mRNA;
- c) contacting the duplex from (b) with one primer having a sequence which is complementary to a portion of the sequence set forth in SEQ ID NO:1 and a second primer having a sequence which comprises a different portion of the sequence set forth in SEQ ID NO:1;
- d) amplifying the nucleic acid from (c) using a

Applicants: Ron S. Israeli, et al.

Serial No.: 08/466,381 Filed : June 6, 1995

Page 4

polymerase chain reaction to obtain an amplification product;

- e) contacting the amplification product of (d) under hybridizing conditions with a labeled nucleic acid probe which: 1) is at least 15 nucleotides in length; 2) hybridizes specifically to a nucleic acid having a sequence set forth in SEQ ID NO. 1.;
- f) removing any unbound labeled nucleic acid probe; and
- g) detecting the presence of labeled nucleic acid probe hybridized to the amplification product:
- h) comparing the amount of labeled nucleic acid probe measured in step g) with an amount measured in a negative control sample which does not have micrometastic prostate tumor cells, wherein a higher amount measured in step g) compared to the amount measured in the control sample indicates the detection of [so as to thereby detect] micrometastic prostate tumor cells in the subject.-

J1 --100.

(Amended) A method of detecting micrometastic prostate tumor cells in a subject which comprises:

- a) obtaining a suitable sample of mRNA from the subject;
- b) generating a double-stranded mRNA-cDNA duplex from the mRNA;
- c) contacting the duplex from (b) with one primer having a sequence which is complementary to a portion of the sequence set forth in SEQ ID NO:1 and a second primer having a sequence which comprises a different portion of the sequence set forth in SEQ ID NO:1;

Applicants: Ron S. Israeli, et al.

Serial No.: 08/466,381 Filed : June 6, 1995

Page 5

- d) amplifying the nucleic acid from (c) using a polymerase chain reaction to obtain an amplification product;
- e) contacting the amplification product of (d) under hybridizing conditions with a labeled nucleic acid probe which: 1) is at least 15 nucleotides in length; and 2) hybridizes specifically to a nucleic acid having a sequence complementary to the DNA sequence set forth in SEQ ID NO:1.;
- f) removing any unbound labeled nucleic acid probe; and
- g) detecting the presence of labeled nucleic acid probe hybridized to the amplification product:
- h) comparing the amount of labeled nucleic acid probe measured in step g) with an amount measured in a negative a control sample which does not have micrometastic prostate tumor cells, wherein a higher amount measured in step g) compared to the amount measured in the control sample indicates the detection of [so as to thereby detect] micrometastic prostate tumor cells in the subject.-

## **REMARKS**

Claims 97-103 are pending in the subject application. Applicants have hereinabove amended claims 97-100. Support for these amendments may be found <u>inter alia</u> in the specification on page 86, lines 15-16. This amendment does not involve any issue of new matter. Therefore, entry of this amendment is respectfully requested such that claims 97-103 will be pending.

31 Cont